

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 26, 2002, 20:33:06 ; Search time 1934 Seconds
(without alignments)
4836.293 Million cell updates/sec

Title: US-09-840-795-18_COPY_78_770

Perfect score: 693

Sequence: 1 atgagttgcacgaagaatga.....agcagcaggggcctgaatg 693

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hic:*
9: gp_estl:*
10: gp_estl:*
11: gp_hic:*
12: gp_gss:*
13: em_gss_hum:*
14: em_gss_inu:*
15: em_gss_pin:*
16: em_gss_vrtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	403.2	58.2	689	9	BB219800 BB219800
2	362.2	52.3	951	10	BM013263 603635039
3	359.2	51.8	697	9	BB627119 BB627119
4	327.8	47.3	680	9	BB651661 BB651661
5	291	42.0	614	9	BB637179 BB637179
6	186.8	27.0	459	9	BB858916 BB858916
7	169.6	24.5	442	10	BE554624 BB554624
8	148.2	21.4	680	9	BB653265 BB653265
9	135	19.5	616	9	BB650696 BB650696
10	133.2	19.2	395	10	BE306459 601103459
11	122.4	17.7	589	10	BM004238 BB004238
12	110.4	15.9	894	10	BT662288 BT662288
13	100.6	14.5	932	10	BT191939 BT191939
14	94	13.6	519	9	BB857078 BB857078
15	91.4	13.2	534	10	BE757704 212225 MA
16	86	12.4	566	10	BC635626 354836 MA
17	79.2	11.4	258	9	BB542020 BB542020

18	76.6	11.1	401	9	AA003356
19	71.8	10.4	526	9	BB856841 BB856841
20	67	9.7	358	9	AA036247 AA036247
21	64.4	9.3	499	9	BB858206 BB858206
22	60.2	8.7	678	9	BB641271 BB641271
23	59.6	8.6	673	10	BT904967 BT904967
24	58.2	8.4	1110	12	CNS0507C
25	57	8.2	626	9	BB652914 BB652914
26	52.4	7.6	275	9	AV111112 AV111112
27	47.6	6.9	282	9	AL036000
28	46	6.6	612	12	AQ021525
29	42.2	6.1	670	10	BT523347
30	39.6	5.7	708	9	AL655137
31	39.2	5.7	803	9	AL569668
32	38.6	5.6	547	10	BG897869
33	38.6	5.6	568	10	BM010615
34	38.6	5.6	641	10	BE276747
35	38.6	5.6	706	9	AL580892
36	38.6	5.6	713	10	BG752816
37	38.6	5.6	817	10	BC575868
38	38.6	5.6	884	10	BG696700
39	38.6	5.6	889	10	BT522640
40	38.6	5.6	939	10	BT520358
41	38.6	5.6	970	9	AL551177
42	38.6	5.6	1048	10	BM458980
43	38.6	5.6	1067	10	BF037815
44	38.6	5.6	1096	10	BG391978
45	38.6	5.6	1176	10	BT911227

ALIGNMENTS

RESULT 1
LOCUS BB219800
DEFINITION BB219800 RIKEN full-length enriched, adult male aorta and vein mus
musculus cDNA clone A530057a22 3', mRNA sequence.
VERSION BB219800
KEYWORDS GI:16353450
SOURCE BB219800.2
ORGANISM house mouse.
EST.
REFERENCE 1 (bases 1 to 689)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanaoka,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okada,K., Okazaki,Y., Okido,T., Saito,K., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyu,T., Muramatsu,M., and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jun 30, 2000 this sequence version replaced gi:8884753.
Contact: Yoshinori Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Maitani,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

VERSION BB637179.1 GI:16472964
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Aukawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hoti,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muraiatsu,M., and Hayashizaki,Y.
RIKEN Mouse ESTs (Arawaka,T., et al. 2001)
COMMENT Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resesc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Kono,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Y., and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedic: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamana,K., Aizawa
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
source
Location/Qualifiers
1. 614
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A530057A22"
/clone_1ib="RIKEN full-length enriched, adult male aorta
and vein"
/sex="male"
/tissue-type="aorta and vein"
/dev-stage="adult"
/lab_host="DH10B"
/note="Site.1: SalI; Site.2: BamHI. cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCAGACCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATTCGAGTTAATTAATTAATTCACCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from lambda
FLC I."

BASE COUNT 166 a 145 c 156 g 147 t
ORIGIN
Query Match 42.0%; Score 291; DB 9; Length 614;
Best Local Similarity 85.9%; Pred. No. 9, 9e-72;
Matches 346; Conservative 0; Mismatches 55; Indels 2; Gaps 2;
1 ATGATTTGCCAAGAAATGATGCTACTGGACCAATGGGAGGCTGTGACCTGCCAACCG 60
182 ATGATTTGCCAAGAAATGATGCTACTGGACCAATGGGAGGCTGTGACCTGCCAACCG 241
61 TGTGCTCTGAGACAGGAGCTATCCAGATTTGTTATGAGAGGTGAGATGCTTAC 120
242 TGTGCTCTGAGACAGGAGCTATCCAGATTTGTTATGAGAGGTGAGATGCTTAC 301
121 TGCACAGCTGCTGCTCTGCTGAGTACAAAGACAGTGGGGCCACCAAAATGTACAGT 180
302 TGCATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
181 TGCATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
362 TGCATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
241 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
422 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
301 GACCAAGAGTGCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359
482 GACCAAGAGTGCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
360 CCAAGTGCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 401
542 CCAAGTGCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584

RESULT 6
BB858916 459 bp mRNA linear EST 26-NOV-2001
DEFINITION BB858916 RIKEN full-length enriched, kidney CCL-142 RAG cDNA Mus
ACCESSION BB858916
VERSION BB858916
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Aukawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hoti,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
Watanabe,M., Tsunishi,A., Muramatsu,M., and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)
COMMENT Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resesc.riken.go.jp,

URL: [http://genome.gsc.riken.go.jp](http://genome.gsc.riken.go.jp/Carninci.P., Shibata.Y., Hayatsu.N., Sugahara.Y., Shibata.K., Itoh.M., Kono.H., Okazaki.Y., Muramatsu.M. and Hayashizaki.Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi.K., Fujiwaka.S., Inoue.K., Togawa.Y., Izawa.M., Ohara.E., Watabiki.M., Yoneda.Y., Ishikawa.T., Ozawa.K., Tanaka.T., Matsuura.S., Kawai.J., Okazaki.Y., Muramatsu.M., Inoue.Y., Kira.A. and Hayashizaki.Y. RIKEN Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Kono.H., Fukunishi.Y., Shibata.K., Itoh.M., Carninci.P., Sugahara.Y. and Hayashizaki.Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (<a href=)) for further details.

FEATURES

SOURCE

Location/Qualifiers

1..459

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="G43003D23"

/clone_lib="RIKEN full-length enriched, kidney CCL-142 RAG

/tissue_type="kidney"

/cell_line="CCL-142 RAG"

BASE COUNT 136 a 98 c 116 g 109 t

ORIGIN

Query Match 27.0%; Score 186.8; DB 9; Length 459;

Best Local Similarity 86.6%; Pred. No. 3.2e-42;

Matches 206; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

1 ATGATTTGCCAAGAAATGACTGAGCAATGGGAGCGGTGTGTCACCTGCCAACGG 60

222 ATGATTTGCCAAGAAATGACTGAGCAATGGGAGCGGTGTGTCACCTGCCAACCA 281

61 TGTGCTCTGGACAGAGACTATCCAGATGTTGTTATGGAGAGGTGGAGATCCCTAC 120

282 TGTGCTCTGGACAGAGACTATCCAGATGTTGTTATGGAGAGGTGGAGATCCACAC 341

121 TGCACAGCTGCGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 180

342 TGCATAGTCTGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 401

181 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 238

402 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 459

Db 342 TGCATAGTCTGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 401

181 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 238

402 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 459

Db 342 TGCATAGTCTGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 401

181 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 238

402 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 459

Db 342 TGCATAGTCTGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 401

181 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 238

402 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 459

Db 342 TGCATAGTCTGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 401

181 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 238

402 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 459

Db 342 TGCATAGTCTGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 401

181 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 238

402 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 459

Db 342 TGCATAGTCTGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 401

181 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 238

402 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 459

Db 342 TGCATAGTCTGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 401

181 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 238

402 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 459

Db 342 TGCATAGTCTGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 401

181 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 238

402 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 459

Db 342 TGCATAGTCTGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 401

181 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 238

Email: cqabp-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1056280
Seq primer: -40RP from Glibco
High quality sequence stop: 425.

FEATURES

SOURCE

Location/Qualifiers

1..442

/organism="Mus musculus"

/strain="FVB/N-3"

/db_xref="taxon:10090"

/clone="IMAGE:3153524"

/clone_lib="NCI CGAP_Mam2"

/tissue_type="tumor, biopsy sample"

/dev_stage="5 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT

123 a 104 c 114 g 101 t

ORIGIN

Query Match 24.5%; Score 169.6; DB 10; Length 442;

Best Local Similarity 85.5%; Pred. No. 2.4e-37;

Matches 212; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

1 ATGATTTGCCAAGAAATGACTGAGCAATGGGAGCGGTGTGTCACCTGCCAACCG 60

197 ATGATTTGCCAAGAAATGACTGAGCAATGGGAGCGGTGTGTCACCTGCCAACCA 255

61 TGTGCTCTGGACAGAGACTATCCAGATGTTGTTATGGAGAGGTGGAGATCCCTAC 120

256 TGTGCTCTGGACAGAGACTATCCAGATGTTGTTATGGAGAGGTGGAGATCCACAC 315

121 TGCACAGCTGCGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 180

316 TGCATAGTCTGCTCTGTCGAGATCAAAAGCAGCTGGGGCAGACCAAAATGTAGAGT 374

181 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 240

375 TGCATACCTGCTGCTGTCATCATCGTGTTCAGAGTCACTGCACAGCTACCTCTTA 434

241 GCTGCTCTG 248

435 CCTATCTG 442

Db 435 CCTATCTG 442

241 GCTGCTCTG 248

435 CCTATCTG 442

Db 435 CCTATCTG 442

241 GCTGCTCTG 248

435 CCTATCTG 442

Db 435 CCTATCTG 442

241 GCTGCTCTG 248

435 CCTATCTG 442

Db 435 CCTATCTG 442

241 GCTGCTCTG 248

435 CCTATCTG 442

Db 435 CCTATCTG 442

241 GCTGCTCTG 248

435 CCTATCTG 442

Db 435 CCTATCTG 442

241 GCTGCTCTG 248

435 CCTATCTG 442

Db 435 CCTATCTG 442

241 GCTGCTCTG 248

435 CCTATCTG 442

Db 435 CCTATCTG 442

241 GCTGCTCTG 248

435 CCTATCTG 442

Db 435 CCTATCTG 442

241 GCTGCTCTG 248

435 CCTATCTG 442

Db 435 CCTATCTG 442

241 GCTGCTCTG 248

435 CCTATCTG 442

Db 435 CCTATCTG 442

241 GCTGCTCTG 248

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@isc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

e mouse tissues.

FEATURES

source

Location/Qualifiers
1. 680
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="D930037D22"
/clone_lib="RIKEN full-length enriched, 15 days embryo
head"
/sex="mixed"
/tissue_type="head"
/dev_stage="15 days embryo"
/lab_host="DH10B"
/note="Site.1: Salt: Site.2: BamHI: cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 15'
GAGAGAGAGATTCGAGTATTAATTAATCCCGCCCCCCCC 3'. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I"

BASE COUNT 143 a 192 c 210 g 133 t 2 others
ORIGIN

Query Match 21.4%: Score 148.2; DB 9; Length 680;
Best Local Similarity 59.4%: Pred. No. 3,4e-31;
Matches 249; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

OY 4 GATTGCCAAGAAATGACTGACCAATGGGACGAGGTGTCTCACTCCACGAGTGT 63
DB 253 GATTGGAGGAGAGGAGATTCAGATTCATCGGAACACTGTCTCTCCACCAACAGTGC 312
OY 64 GTCTGAGGAGAGGAGATTCAGATTCATCGGAACACTGTCTCTCCACCAACAGTGC 123
DB 313 GGACCTGGAGATTCAGATTCATCGGAACACTGTCTCTCCACCAACAGTGC 372

OY 124 ACAGCTGCGCTCTCTGAGTACAAAGACGCTGGGGCCACCAACAAATGTCAGATTGC 183
DB 373 GTGCCCTGACGGCCGACCGGATTCAGGAAGACTGGGGGTTTTCAGGAAGTGAAGCCATTGT 432
OY 184 ATGACCTGTGCTGTCAATCATGCTGTTCAGAGAGTCACTGACACAGTCTTAATGCT 243
DB 433 GCGGACTGTGCGGTGTGAGAACCGTTTCAGAGGGCCAACTGCTCAGACACAGTATGCT 492
OY 244 GTCTGAGGAGAGTGTGGTCCAGAGTTCACCAAGAACAGCATTTGAGAGCTTCAGAC 303
DB 493 GTCTGCGGAGACTGCTGCGCAGAGATTATCCGGAAGACCAAACTGTTGGTTTCAAGAC 552
OY 304 CAGAGTGCATCCCTGCGCAGAGACACCCCACTGTAGTTCATATGCTCTTCAG 363
DB 553 ATGAGTGTGCTGCTGCGGAGACACCTGCTCCCTACACACCCAGTCTTACAGGAG 612
OY 364 TTGAGCTTACTGAGGAGATGACACCCAGTGGCCCCCTCAGAGAGCCACATTTGTCG 422
DB 613 GTGACCTTGTGAAGATCTCTCCACACGCTGAGCCCTGCGGACACGGGCTGCTGC 671

RESULT 9 616 bp mRNA linear EST 26-OCT-2001
BB650696
LOCUS BB650696
DEFINITION BB650696 RIKEN full-length enriched, 0 day neonate cerebellum Mus
ACCESSION BB650696
VERSION BB650696.1 GI:16484951
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 616)
AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Kondo, H., Kouda
, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M., and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
TITLE Unpublished (2001)
JOURNAL Contact: Yoshinide Hayashizaki
COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@isc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 932)	NIH-MGC	http://mgc.nci.nih.gov/	
1	(bases 1 to 932)	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)	
Contact:	Robert Strausberg, Ph.D.	Email:	cgabbs-r@mail.nih.gov	
Tissue Procurement:	Life Technologies, Inc.	CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by:	Incyte Genomics, Inc.	Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	
http://image.llnl.gov		Plate:	LLAM11627	row: 0 column: 18
High quality sequence start:	28	High quality sequence stop:	723.	
Location/Qualifiers	1..932			
/organism="Homo sapiens"		/db_xref="taxon:9606"		
/clone="IMAGE:5248745"		/clone_lib="NIH_MGC_121"		
/lab_host="DH10B"		/note="Organ: brain; Vector: pcwv-SPORT6; Site:1: NotI; Site-2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note this is a NIH MGC Library."		
BASE COUNT	242 a	222 c	234 g	234 t
ORIGIN				
Query Match	14.5%	Score 100.6;	DB 10;	Length 932;
Best Local Similarity	61.0%;	Pred. No. 1.3e-17;		
Matches 197;	Conservative 0;	Mismatches 124;	Indels 2;	Gaps 2;
OY	19	GAGTCTGGGACCAATMGGGGACGGGTGTGCACCTGCGCAACGGTGTGCTTGGACAGAG 78		
DB	448	GAATTCAGGGATCGGCTGTGGAACCTGTGTCCTTGCAACCACTGTGGCCAGCATGAG 507		
OY	79	CTATCCAAAGATTGTTGATTATGAGAGGGGTGAGATGCTTACTGCACAGCCCTGCCT 138		
DB	508	TGTCTAAGAGATGTGGCTTCGGCTATGGGGAGAGATGCACAGTGTGTACGTCGCCGGC 567		
OY	139	CGCAGGTCAAAAGACAGCTGGGGCCACCAATATGTAG-AGTTGCATCCTGTGTGT 197		
DB	568	CACAGGTTTCAGAGAGACTTGGGGCTTCAGAAATCAAGACCCTGTGTGAGCTGCCAGT 627		
OY	198	CATCAATCGTGTTCAGAAAGTCA-AC TGACAGCTATACCTTAACTGTCGTGTGGAGCT 256		
DB	628	GGTGAACCGCTTCAGAAAGCAACATTGTTGACGCCACCAAGTATCCATCTGGAGACT 687		
OY	257	GTTTCCCAAGTTCTTACCGAAAGACACCATTTGAGAGCGCTTCAGAGCAAGAGATCAATC 316		
DB	688	GCTTCCAGGATCTCATGAGAAAGAAACATTGTCGGCTATCAAGACATMGAGTGTGTGC 747		
OY	317	CGTGCAGAGACAGACCCCCAC 339		
DB	748	CTGTGAGAGACCCCTCCATC 770		
RESULT 14				
LOCUS	BB857078	519 bp	mrna	linear
DEFINITION	BB857078 RIKEN full-length enriched, B16 F10Y cells Mus musculus			EST 26-NOV-2001
ACCESSION	BB857078			
VERSION	BB857078.1	GI:17098532		

	KEYWORDS	EST.
	SOURCE	house mouse.
	ORGANISM	Mus musculus
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 519)
	AUTHORS	Akimura,T., Atakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Imotani,K., Ishii Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Koude,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa A., Takahashi,F., Takaku-Akahira,S., Tanaka,Y., Tomaru,A., Toyota,T., Wataniki,A., Yasunishi,A., Yamamatsu,M. and Hayashizaki,Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)
	JOURNAL	Unpublished (2001)
	COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsr.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagdi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuo S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
	FEATURES	e mouse tissues.
	SOURCE	Location/Qualifiers 1..519 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="G370041G09" /clone_1lb="RIKEN full-length enriched, B16 F10Y cells" /cell_type="B16 F10Y cells"
	BASE COUNT	112 a 138 c 167 g 102 t
	ORIGIN	
	Query Match	13.6%; Prod. 94; DB 9; Length 519;
	Best local similarity	63.3%; Pctid. No. 7.2e-16;
	Matches 176; Conservative 0; Mismatches 100; Indels 2; Gaps 2;	
0Y	4	GATTGCCAGAAATAGTACTGGACCAATGGGAGCGTGTCATCTGCCAACGTGT 63
Db	242	GATTGCAGCGAGCAGCATTCAGATCGATCGTAAGAATCTGCTCCATCAACAAGTGC 301
0Y	64	GGTCTGCACGAGGAGCATCAAGATTTGGTTATGGAAGAGGTGAATGCTTACTGC 123
Db	302	GGACCTGCAGTAGGAGTGT-CAAGCAATGTGCTCTCGGCTATGGGAGATGACAGTGT 360
0Y	124	ACAGCCTGCCCCCTCTCCAGGTACCAAAAGACAGTGGGGCCACCACCAAAATGTCAGATGTC 183
Db	361	GTGGCCCTGCAGGCGCCGCAACGGTTAAGGAATA-CTGGGCTTTCCAGAAAGTGAAGCATAT 419

OY	184	ATCACGCTGCTGTCATCAATACGTTGTCAGAAAGTCACACAGCTACCTTAATGCT	24.3
Db	420	GCGACGTGTGCGTGTGTGAACCCGTTTCAGAGGSCAAATCTCTCACACACCATGATGCT	47.9
OY	244	GTCGTGGGACCTGTTGCCAGGTTCTACCGAAAGAC	28.1
Db	480	GTCGTGGGACCTGCTTCCAGGATTTTACCGGAAGAC	51.7

RESULT					
15					
LOCUS	BET57704				
DEFINITION	BET57704	534 bp	mRNA	linear	EST 25-APR-2001
ACCESSION	212222	MARC	2BOV Bos taurus	CDNA 5'	, mRNA sequence.
VERSION	BET57704				
KEYWORDS	BET57704.1				GI:10171696
SOURCE	EST.				
COM.					

TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA
JOURNAL	libraries and construction of a gene index for cattle
MEDLINE	Genome Res. 11 (4), 626-630 (2001)
COMMENT	21180013
	Contact: Smith TPL

BASE COUNT	122 a	117 c	171 g	124 t
ORIGIN				

Db	409	GTGAAGTCCCGCCGCGCAGGTTCAAGAGAGACTGGGGCTCTCAGAAAGTGCAAGCCCTGC	468
QY	184	ATCACTGTCGCTGTCAATCAATCGTTCAGAGAGGTCAAGTGCACAGTACTCTAAATGCT	243
Db	469	CTGACATGCGCCCTGCTGAGCGGCTTCACAGAGGCCAATCTCTGGCCATCGGAGACCC	528
QY	244	GTCCTG 248	
Db	529	GTCCTG 533	

Search completed: October 27, 2002, 02:39:57
Job time : 1942 secs

THIS PAGE BLANK (USPTO)